

SEQUENCE LISTING

<110> Yoshinaga, Steven K.

<120> NOVEL POLYPEPTIDES INVOLVED IN IMMUNE RESPONSE

<130> A-579-C

<140> 09/264,527

<141> 1999-03-08

<160> 35

<170> PatentIn Ver. 2.1

<210> 1

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<212> DNA

<213> mouse

<220>

<221> CDS

<222> Complement((1)..(600))

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ctt tta aca gga gaa atc aat ggc tcc gcc gat cat agg atg ttt tca 96
Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser
20 25 30

ttt cac aat gga ggt gta cag att tct tgt aaa tac cct gag act gtc 144
Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val
35 40 45

cag cag tta aaa atg cga ttg ttc aga gag aga gaa gtc ctc tgc gaa 192
Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu
50 55 60

ctc acc aag acc aag gga agc gga aat gcg gtg tcc atc aag aat cca 240
Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro
65 70 75 80

atg ctc tgt cta tat cat ctg tca aac aac agc gtc tct ttt ttc cta 288
Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
85 90 95

aac aac cca gac agc tcc cag gga agc tat tac ttc tgc agc ctg tcc 336
Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser
100 105 110

att ttt gac cca cct cct ttt caa gaa agg aac ctt agt gga gga tat 384
Ile Phe Asp Pro Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr
115 120 125

ttg cat att tat gaa tcc cag ctc tgc tgc cag ctg aag ctc tgg cta 432
Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
130 135 140

ccc gta ggg tgt gca gct ttc gtt gtg gta ctc ctt ttt gga tgc ata 480
Pro Val Gly Cys Ala Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile
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0926420.1.2800

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Asp	Ser	Asn 35	Glu	Val	Ser	Leu	Ser 40	Cys	Arg	Tyr	Ser	Tyr 45	Asn	Leu	Leu
Ala	Lys 50	Glu	Phe	Arg	Ala	Ser 55	Leu	Tyr	Lys	Gly	Val 60	Asn	Ser	Asp	Val
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gtt tgg aag aag ctc cat gtt tct agc ggg ttc ttt tct ggt ctt ggt 96
Val Trp Lys Lys Leu His Val Ser Ser Gly Phe Phe Ser Gly Leu Gly
20 25 30

ctg ttc ttg ctg ctg ttg agc agc ctc tgt gct gcc tct gca gag act 144
Leu Phe Leu Leu Leu Leu Ser Ser Leu Cys Ala Ala Ser Ala Glu Thr
35 40 45

gaa gtc ggt gca atg gtg ggc agc aat gtg gtg ctc agc tgc att gac 192
Glu Val Gly Ala Met Val Gly Ser Asn Val Val Leu Ser Cys Ile Asp
50 55 60

ccc cac aga cgc cat ttc aac ttg agt ggt ctg tat gtc tat tgg caa 240
Pro His Arg Arg His Phe Asn Leu Ser Gly Leu Tyr Val Tyr Trp Gln
65 70 75 80

atc gaa aac cca gaa gtt tcg gtg act tac tac ctg cct tac aag tct 288
Ile Glu Asn Pro Glu Val Ser Val Thr Tyr Tyr Leu Pro Tyr Lys Ser
85 90 95

cca ggg atc aat gtg gac agt tcc tac aag aac agg ggc cat ctg tcc 336
Pro Gly Ile Asn Val Asp Ser Ser Tyr Lys Asn Arg Gly His Leu Ser
100 105 110

ctg gac tcc atg aag cag ggt aac ttc tct ctg tac ctg aag aat gtc 384
Leu Asp Ser Met Lys Gln Gly Asn Phe Ser Leu Tyr Leu Lys Asn Val
115 120 125

acc cct cag gat acc cag gag ttc aca tgc cgg gta ttt atg aat aca 432
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<211> 322
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<213> mouse
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<210> 8
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<400> 8
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Leu	Cys	Cys	Val	Glu	Asn	Val	Ala	Leu	His	Gln	Asn	Ile	Thr	Ser	Ile
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		275					280					285			
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Leu	Phe	Xaa 35	Leu	Leu	Xaa	Xaa	Xaa 40	Ser	Xaa	Xaa	Xaa	Xaa 45	Xaa	Xaa	Xaa
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Gln	Xaa	Xaa	Xaa	Xaa 85	Xaa	Val	Xaa	Xaa	Xaa 90	Xaa	Xaa	Leu	Xaa	Xaa 95	Xaa
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Xaa	Leu	Xaa 115	Xaa	Xaa	Xaa	Xaa	Xaa 120	Xaa	Xaa	Ser	Leu	Xaa 125	Xaa	Xaa	Xaa
Xaa	Xaa 130	Xaa	Xaa	Asp	Xaa	Xaa 135	Xaa	Xaa	Xaa	Cys	Xaa 140	Val	Xaa	Xaa	Xaa
Xaa 145	Xaa	Xaa	Xaa	Xaa	Xaa 150	Xaa	Xaa	Xaa	Xaa	Xaa 155	Xaa	Val	Xaa	Leu	Xaa 160
Xaa	Xaa	Ala	Xaa	Phe 165	Ser	Thr	Pro	Xaa	Ile 170	Xaa	Xaa	Ser	Xaa	Xaa 175	Xaa
Xaa	Xaa	Xaa	Xaa 180	Xaa	Arg	Xaa	Xaa	Thr 185	Cys	Xaa	Xaa	Xaa	Xaa 190	Gly	Xaa
Pro	Xaa	Pro 195	Xaa	Xaa	Xaa	Trp	Xaa 200	Xaa	Asn	Xaa	Xaa	Xaa 205	Xaa	Xaa	Xaa
Ile	Xaa 210	Thr	Xaa	Xaa	Xaa	Xaa 215	Xaa	Xaa	Xaa	Xaa	Xaa 220	Xaa	Xaa	Xaa	Xaa
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Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val Xaa Val Xaa Val Xaa Xaa
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 <212> DNA
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<220>
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 cga gct gat act cag gag aag gaa gtc aga gcg atg gta ggc agc gac 96
 Arg Ala Asp Thr Gln Glu Lys Glu Val Arg Ala Met Val Gly Ser Asp
 20 25 30
 gtg gag ctc agc tgc gct tgc cct gaa gga agc cgt ttt gat tta aat 144
 Val Glu Leu Ser Cys Ala Cys Pro Glu Gly Ser Arg Phe Asp Leu Asn
 35 40 45
 gat gtt tac gta tat tgg caa acc agt gag tcg aaa acc gtg gtg acc 192
 Asp Val Tyr Val Tyr Trp Gln Thr Ser Glu Ser Lys Thr Val Val Thr
 50 55 60
 tac cac atc cca cag aac agc tcc ttg gaa aac gtg gac agc cgc tac 240
 Tyr His Ile Pro Gln Asn Ser Ser Leu Glu Asn Val Asp Ser Arg Tyr
 65 70 75 80
 cgg aac cga gcc ctg atg tca ccg gcc ggc atg ctg cgg gcc gac ttc 288
 Arg Asn Arg Ala Leu Met Ser Pro Ala Gly Met Leu Arg Gly Asp Phe
 85 90 95
 tcc ctg cgc ttg ttc aac gtc acc ccc cag gac gag cag aag ttt cac 336
 Ser Leu Arg Leu Phe Asn Val Thr Pro Gln Asp Glu Gln Lys Phe His
 100 105 110
 tgc ctg gtg ttg agc caa tcc ctg gga ttc cag gag gtt ttg agc gtt 384
 Cys Leu Val Leu Ser Gln Ser Leu Gly Phe Gln Glu Val Leu Ser Val
 115 120 125
 gag gtt aca ctg cat gtg gca gca aac ttc agc gtg ccc gtc gtc agc 432
 Glu Val Thr Leu His Val Ala Ala Asn Phe Ser Val Pro Val Val Ser
 130 135 140
 gcc ccc cac agc ccc tcc cag gat gag ctc acc ttc acg tgt aca tcc 480
 Ala Pro His Ser Pro Ser Gln Asp Glu Leu Thr Phe Thr Cys Thr Ser
 145 150 155 160
 ata aac ggc tac ccc agg ccc aac gtg tac tgg atc aat aag acg gac 528

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tgg Trp	agc Ser	atc Ile	ctg Leu 260	gct Ala	gtc Val	ctg Leu	tgc Cys	ctg Leu 265	ctt Leu	gtg Val	gtc Val	gtg Val	gcg Ala 270	gtg Val	gcc Ala	816
ata Ile	ggc Gly 275	tgg Trp	gtg Val	tgc Cys	agg Arg	gac Asp	cga Arg 280	tgc Cys	ctc Leu	caa Gln	cac His	agc Ser 285	tat Tyr	gca Ala	ggt Gly	864
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Val	Glu	Leu 35	Ser	Cys	Ala	Cys	Pro 40	Glu	Gly	Ser	Arg	Phe 45	Asp	Leu	Asn	
Asp	Val 50	Tyr	Val	Tyr	Trp	Gln 55	Thr	Ser	Glu	Ser	Lys 60	Thr	Val	Val	Thr	
Tyr 65	His	Ile	Pro	Gln	Asn 70	Ser	Ser	Leu	Glu	Asn 75	Val	Asp	Ser	Arg	Tyr 80	
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Cys	Leu	Val 115	Leu	Ser	Gln	Ser	Leu 120	Gly	Phe	Gln	Glu	Val 125	Leu	Ser	Val	
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Ala Pro His Ser Pro Ser Gln Asp Glu Leu Thr Phe Thr Cys Thr Ser
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165 170 175
Asn Ser Leu Leu Asp Gln Ala Leu Gln Asn Asp Thr Val Phe Leu Asn
180 185 190
Met Arg Gly Leu Tyr Asp Val Val Ser Val Leu Arg Ile Ala Arg Thr
195 200 205
Pro Ser Val Asn Ile Gly Cys Cys Ile Glu Asn Val Leu Leu Gln Gln
210 215 220
Asn Leu Thr Val Gly Ser Gln Thr Gly Asn Asp Ile Gly Glu Arg Asp
225 230 235 240
Lys Ile Thr Glu Asn Pro Val Ser Thr Gly Glu Lys Asn Ala Ala Thr
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35 40 45
Asn Ser Ser Leu Glu Asn Val Asp Ser Arg Tyr Arg Asn Arg Ala Leu
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Met Ser Pro Ala Gly Met Leu Arg Gly Asp Phe Ser Leu Arg Leu Phe
65 70 75 80
Asn Val Thr Pro Gln Asp Glu Gln Lys Phe His Cys Leu Val Leu Ser
85 90 95
Gln Ser Leu Gly Phe Gln Glu Val Leu Ser Val Glu Val Thr Leu His
100 105 110
Val Ala Ala Asn Phe Ser Val Pro Val Val Ser Ala Pro His Ser Pro
115 120 125
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Trp	Gln	Ile 35	Glu	Asn	Pro	Glu	Val 40	Ser	Val	Thr	Tyr	Tyr 45	Leu	Pro	Tyr
Lys	Ser 50	Pro	Gly	Ile	Asn	Val 55	Asp	Ser	Ser	Tyr	Lys 60	Asn	Arg	Gly	His
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Arg	Val	Ala 115	Ala	Asn	Phe	Ser	Thr 120	Pro	Val	Ile	Ser	Thr 125	Ser	Asp	Ser
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Tyr 145	Pro	Glu	Pro	Asn	Leu 150	Tyr	Trp	Ile	Asn	Thr 155	Thr	Asp	Asn	Ser	Leu 160
Ile	Asp	Thr	Ala	Leu 165	Gln	Asn	Asn	Thr	Val 170	Tyr	Leu	Asn	Lys	Leu 175	Gly
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Trp	Gln	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Val	Thr	Tyr	Xaa	Xaa	Pro	Xaa	
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	50					55					60					
Xaa	Ser	Xaa	Xaa	Xaa	Met	Xaa	Xaa	Gly	Xaa	Phe	Ser	Leu	Xaa	Leu	Xaa	
65					70					75					80	
Asn	Val	Thr	Pro	Gln	Asp	Xaa	Gln	Xaa	Phe	Xaa	Cys	Xaa	Val	Xaa	Xaa	
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Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Leu	Xaa	Xaa	Xaa	Val	Xaa	Leu	
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Xaa	Val	Ala	Ala	Asn	Phe	Ser	Xaa	Pro	Val	Xaa	Ser	Xaa	Xaa	Xaa	Ser	
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145					150					155					160	
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<400> 16															
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cgaggtctcc gcccgcacc atg cgg ctg ggc agt cct gga ctg ctc ttc ctg															232
Met Arg Leu Gly Ser Pro Gly Leu Leu Phe Leu															
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Leu Phe Ser Ser Leu Arg Ala Asp Thr Gln Glu Lys Glu Val Arg Ala															
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Met Val Gly Ser Asp Val Glu Leu Ser Cys Ala Cys Pro Glu Gly Ser															
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Lys Thr Val Val Thr Tyr His Ile Pro Gln Asn Ser Ser Leu Glu Asn															
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Arg	Asn	Arg	Ala	Leu	Met	Ser	Pro	Ala	Gly	Met	Leu	Arg	Gly	Asp	Phe
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Ser	Leu	Arg	Leu	Phe	Asn	Val	Thr	Pro	Gln	Asp	Glu	Gln	Lys	Phe	His
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Cys	Leu	Val	Leu	Ser	Gln	Ser	Leu	Gly	Phe	Gln	Glu	Val	Leu	Ser	Val
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Ile	Asn	Gly	Tyr	Pro	Arg	Pro	Asn	Val	Tyr	Trp	Ile	Asn	Lys	Thr	Asp
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Met	Arg	Gly	Leu	Tyr	Asp	Val	Val	Ser	Val	Leu	Arg	Ile	Ala	Arg	Thr
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Lys	Ile	Thr	Glu	Asn	Pro	Val	Ser	Thr	Gly	Glu	Lys	Asn	Ala	Ala	Thr
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Arg	Asn	Arg	Ala	Leu	Met	Ser	Pro	Ala	Gly	Met	Leu	Arg	Gly	Asp	Phe	
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Ser	Leu	Arg	Leu	Phe	Asn	Val	Thr	Pro	Gln	Asp	Glu	Gln	Lys	Phe	His	
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Cys	Leu	Val	Leu	Ser	Gln	Ser	Leu	Gly	Phe	Gln	Glu	Val	Leu	Ser	Val	
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Asn	Ser	Leu	Leu	Asp	Gln	Ala	Leu	Gln	Asn	Asp	Thr	Val	Phe	Leu	Asn	
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Met	Arg	Gly	Leu	Tyr	Asp	Val	Val	Ser	Val	Leu	Arg	Ile	Ala	Arg	Thr	
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	210					215					220					
Asn	Leu	Thr	Val	Gly	Ser	Gln	Thr	Gly	Asn	Asp	Ile	Gly	Glu	Arg	Asp	
225					230					235					240	
Lys	Ile	Thr	Glu	Asn	Pro	Val	Ser	Thr	Gly	Glu	Lys	Asn	Ala	Ala	Thr	
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Trp	Ser	Ile	Leu	Ala	Val	Leu	Cys	Leu	Leu	Val	Val	Val	Ala	Val	Ala	
			260					265					270			
Ile	Gly	Trp	Val	Cys	Arg	Asp	Arg	Cys	Leu	Gln	His	Ser	Tyr	Ala	Gly	
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<400> 19

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Leu	Phe	Leu	Leu	Leu	Leu	Ser	Ser	Leu	Cys	Ala	Ala	Ser	Ala	Glu	Thr
		35					40					45			
Glu	Val	Gly	Ala	Met	Val	Gly	Ser	Asn	Val	Val	Leu	Ser	Cys	Ile	Asp
	50					55					60				
Pro	His	Arg	Arg	His	Phe	Asn	Leu	Ser	Gly	Leu	Tyr	Val	Tyr	Trp	Gln
	65				70					75					80
Ile	Glu	Asn	Pro	Glu	Val	Ser	Val	Thr	Tyr	Tyr	Leu	Pro	Tyr	Lys	Ser
				85					90					95	
Pro	Gly	Ile	Asn	Val	Asp	Ser	Ser	Tyr	Lys	Asn	Arg	Gly	His	Leu	Ser
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Thr	Pro	Gln	Asp	Thr	Gln	Glu	Phe	Thr	Cys	Arg	Val	Phe	Met	Asn	Thr
	130					135					140				
Ala	Thr	Glu	Leu	Val	Lys	Ile	Leu	Glu	Glu	Val	Val	Arg	Leu	Arg	Val
	145				150					155					160
Ala	Ala	Asn	Phe	Ser	Thr	Pro	Val	Ile	Ser	Thr	Ser	Asp	Ser	Ser	Asn
				165					170					175	
Pro	Gly	Gln	Glu	Arg	Thr	Tyr	Thr	Cys	Met	Ser	Lys	Asn	Gly	Tyr	Pro
			180					185					190		
Glu	Pro	Asn	Leu	Tyr	Trp	Ile	Asn	Thr	Thr	Asp	Asn	Ser	Leu	Ile	Asp
		195					200					205			
Thr	Ala	Leu	Gln	Asn	Asn	Thr	Val	Tyr	Leu	Asn	Lys	Leu	Gly	Leu	Tyr
	210					215					220				
Asp	Val	Ile	Ser	Thr	Leu	Arg	Leu	Pro	Trp	Thr	Ser	Arg	Gly	Asp	Val
	225				230				235						240
Leu	Cys	Cys	Val	Glu	Asn	Val	Ala	Leu	His	Gln	Asn	Ile	Thr	Ser	Ile
				245					250					255	
Ser	Gln	Ala	Glu	Ser	Phe	Thr	Gly	Asn	Asn	Thr	Lys	Asn	Pro	Gln	Glu
			260					265					270		
Thr	His	Asn	Asn	Glu	Leu	Lys	Val	Leu	Val	Pro	Val	Leu	Ala	Val	Leu
		275					280					285			
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003211 02402260

His Ala

<220>
<223> Description of Artificial Sequence:Synthetic
Oglionucleotide

Figure 1 consists of 12 subplots, labeled (a) through (l), arranged in a 6x2 grid. Each subplot shows the 'Normalized maximum value of the normalized velocity profile' on the y-axis (ranging from 0.0 to 1.0) against the 'Normalized distance from the wall' on the x-axis (ranging from 0.0 to 1.0). The subplots represent different Reynolds numbers (Re): (a) 100, (b) 200, (c) 500, (d) 1000, (e) 2000, (f) 5000, (g) 10000, (h) 20000, (i) 50000, (j) 100000, (k) 200000, and (l) 500000. As the Reynolds number increases, the velocity profiles become more complex, showing a transition from a single peak to multiple peaks and valleys, and the maximum value generally decreases.

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260 265 270
Xaa Xaa Xaa Xaa Xaa Xaa Lys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Ala
275 280 285
Val Leu Xaa Xaa Xaa Xaa Xaa Val Xaa Xaa Xaa Ile Xaa Xaa Xaa Xaa
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Met Lys Ser Gly
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ctc tgg tat ttc ttt ctc ttc tgc ttg cgc att aaa gtt tta aca gga 225
Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg Ile Lys Val Leu Thr Gly
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Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile Phe His Asn Gly
25 30 35
ggg gta caa att tta tgc aaa tat cct gac att gtc cag caa ttt aaa 321
Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val Gln Gln Phe Lys
40 45 50
atg cag ttg ctg aaa ggg ggg caa ata ctc tgc gat ctc act aag aca 369
Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp Leu Thr Lys Thr
55 60 65
aaa gga agt gga aac aca gtg tcc att aag agt ctg aaa ttc tgc cat 417
Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu Lys Phe Cys His
70 75 80
tct cag tta tcc aac aac agt gtc tct ttt ttt cta tac aac ttg gac 465
Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu Tyr Asn Leu Asp
85 90 95 100

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Pro	Pro	Phe	Lys	Val	Thr	Leu	Thr	Gly	Gly	Tyr	Leu	His	Ile	Tyr	Glu		
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Val	Thr	Leu															
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Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val
      35      40
Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp
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Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu
      65      70      75
Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
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Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser
      100      105      110
Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu
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<210> 27
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28

28

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21

18

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